

Serial Number: 09/643,579

ENTERED

OJPE #5
04CU

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☒ other invalid text, such as Extraneous material at end of file
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

RECEIVED
SEP 20 2000
OJPE/JCWS

*Examiner: ~~The above corrections must be communicated to the applicant in the first Office Action.~~ DO NOT send a copy of this form.

3/1/95

OIPE

RAW SEQUENCE LISTING DATE: 09/14/2000
 PATENT APPLICATION: US/09/643,579 TIME: 16:49:22

Input Set : A:\Cpg.pto
 Output Set: N:\CRF3\09142000\I643579.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
 C--> 5 (i) APPLICANT: RICHARD MARTIN BROGLIE
 6 LORIN ROGER DE BONTE
 7 WILLIAM DEAN HITZ
 8 GUO-HUA MIAO
 9 ROBERT STEFAN REITER
 11 (ii) TITLE OF INVENTION: GENES FOR MUTANT MICROSOMAL
 12 FATTY ACID DELTA-12
 13 DESATURASES AND RELATED
 14 ENZYMES FROM PLANTS
 16 (iii) NUMBER OF SEQUENCES: 17
 18 (iv) CORRESPONDENCE ADDRESS:
 19 (A) ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
 20 (B) STREET: 1007 MARKET STREET
 21 (C) CITY: WILMINGTON
 22 (D) STATE: DELAWARE
 23 (E) COUNTRY: U.S.A.
 24 (F) ZIP: 19898
 26 (v) COMPUTER READABLE FORM:
 27 (A) MEDIUM TYPE: FLOPPY DISK
 28 (B) COMPUTER: IBM PC COMPATIBLE
 29 (C) OPERATING SYSTEM: MICROSOFT WINDOWS 95
 30 (D) SOFTWARE: MICROSOFT OFFICE 97
 32 (vi) CURRENT APPLICATION DATA:
 C--> 33 (A) APPLICATION NUMBER: US/09/643,579
 C--> 34 (B) FILING DATE: 22-Aug-2000
 35 (C) CLASSIFICATION:
 37 (vii) PRIOR APPLICATION DATA:
 38 (A) APPLICATION NUMBER: 08/256,047
 39 (B) FILING DATE: NOVEMBER 17, 1992
 41 (viii) ATTORNEY/AGENT INFORMATION:
 42 (A) NAME: Lynne M. Christenbury
 43 (C) REFERENCE/DOCKET NUMBER: BB-1334-A
 45 (ix) TELECOMMUNICATION INFORMATION:
 46 (A) TELEPHONE: (302) 992-5481
 47 (B) TELEFAX: (302) 892-7949
 48 (C) TELEX:
 51 (2) INFORMATION FOR SEQ ID NO: 1:
 53 (i) SEQUENCE CHARACTERISTICS:
 54 (A) LENGTH: 1464 base pairs
 55 (B) TYPE: nucleic acid
 56 (C) STRANDEDNESS: single
 57 (D) TOPOLOGY: linear
 59 (ii) MOLECULE TYPE: cDNA
 61 (ix) FEATURE:
 62 (A) NAME/KEY: CDS

See P. 5

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/643,579

DATE: 09/14/2000
 TIME: 16:49:22

Input Set : A:\Cpg.pto
 Output Set: N:\CRF3\09142000\I643579.raw

63 (B) LOCATION: 130..1281
 C--> 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 67 GGCACGAGCT CGTGCCGAAT TCGGCACGAG AGGAGACAGA GAGAGAGTTT GAGGAGGAGC 60
 69 TTCTTCGTAG GGTTCATCGT TATTAACGTT AAATCTTCAT CCCCCCTAC GTCAGCCAGC 120
 71 TCAAGAAAC ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC 168
 72 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser
 73 1 5 10 216
 75 AAA AAG TCT GAA ACC GAC AAC ATC AAG CGC GTA CCC TGC GAG ACA CCG
 76 Lys Lys Ser Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro
 77 15 20 25 264
 79 CCC TTC ACT GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC
 80 Pro Phe Thr Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe
 81 30 35 40 45 312
 83 AAA CGC TCG ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC
 84 Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile
 85 50 55 60 360
 87 ATA GCC TCC TGC TTC TAC TAC GTC GCC ACC ACT TAC TTC CCT CTC CTC
 88 Ile Ala Ser Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu
 89 65 70 75 408
 91 CCT CAC GCT CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAG
 92 Pro His Pro Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln
 93 80 85 90 456
 95 GGC TGC GTC CTA ACC GGC GTC TGG GTC ATA GCC CAC GAG TGC GGC CAC
 96 Gly Cys Val Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His
 97 95 100 105 504
 99 CAC GCC TTC AGC GAC TAC CAG TGG CTG GAC GAC ACC GTC GGC CTC ATC
 100 His Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile
 101 110 115 120 125 552
 103 TTC CAC TCC TTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT
 104 Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His
 105 130 135 140 600
 107 CGA CGC CAC CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT
 108 Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe
 109 145 150 155 648
 111 GTC CCC AAG AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC
 112 Val Pro Lys Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn
 113 160 165 170 696
 115 AAC CCT TTG GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC
 116 Asn Pro Leu Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly
 117 175 180 185 744
 119 TGG CCT TTG TAC TTA GCC TTC AAC GTC TCG GGG AGA CCT TAC GAC GGC
 120 Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly
 121 190 195 200 205 792
 123 GGC TTC GCT TGC CAT TTC CAC CCC AAC GCT CCC ATC TAC AAC GAC CGT
 124 Gly Phe Ala Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg
 125 210 215 220 840
 127 GAG CGT CTC CAG ATA TAC ATC TCC GAC GCT GGC ATC CTC GCC GTC TGC
 128 Glu Arg Leu Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys
 129 225 230 235

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/643,579

DATE: 09/14/2000
 TIME: 16:49:22

Input Set : A:\Cpg.pto
 Output Set: N:\CRF3\09142000\I643579.raw

```

131 TAC GGT CTC TAC CGC TAC GCT GCT GTC CAA GGA GTT GCC TCG ATG GTC      888
132 Tyr Gly Leu Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val
133      240      245      250
135 TGC TTC TAC GGA GTT CCT CTT CTG ATT GTC AAC GGG TTC TTA GTT TTG      936
136 Cys Phe Tyr Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu
137      255      260      265
139 ATC ACT TAC TTG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAT GAC TCG      984
140 Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser
141 270      275      280      285
143 TCT GAG TGG GAT TGG TTG AGG GGA GCT TTG GCC ACC GTT GAC AGA GAC      1032
144 Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp
145      290      295      300
147 TAC GGA ATC TTG AAC AAG GTC TTC CAC AAT ATC ACG GAC ACG CAC GTG      1080
148 Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val
149      305      310      315
151 GCG CAT CAC CTG TTC TCG ACC ATG CCG CAT TAT CAT GCG ATG GAA GCT      1128
152 Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala
153      320      325      330
155 ACG AAG GCG ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTC GAT GGG      1176
156 Thr Lys Ala Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly
157      335      340      345
159 ACG CCG GTG GTT AAG GCG ATG TGG AGG GAG GCG AAC GAG TGT ATC TAT      1224
160 Thr Pro Val Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr
161 350      355      360      365
163 GTG GAA CCG GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC      1272
164 Val Glu Pro Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn
165      370      375      380
167 AAT AAG TTA TGAAGCAAAG AAGAACTGA ACCTTCTCT TCTATGATTG      1321
168 Asn Lys Leu
170 TCTTTGTTTA AGAAGCTATG TTTCTGTTTC AATAATCTTA ATTATCCATT TTGTTGTGTT      1381
172 TTCTGACATT TTGGCTAAAA TTATGTGATG TTGGAAGTTA GTGTCTAAAA AAAAAAAAAA      1441
174 AAAAAAAAAA AAAAAAAAAA AAA      1464
176 (2) INFORMATION FOR SEQ ID NO: 2:
178 (i) SEQUENCE CHARACTERISTICS:
179 (A) LENGTH: 384 amino acids
180 (B) TYPE: amino acid
181 (D) TOPOLOGY: linear
183 (ii) MOLECULE TYPE: protein
C--> 185 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
187 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
188 1      5      10      15
190 Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
191      20      25      30
193 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
194      35      40      45
196 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ala Ser
197      50      55      60
199 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
200 65      70      75      80

```

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/643,579

DATE: 09/14/2000
 TIME: 16:49:22

Input Set : A:\Cpgg.pto
 Output Set: N:\CRF3\09142000\I643579.raw

```

202 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
203      85      90      95
205 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
206      100      105      110
208 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
209      115      120      125
211 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
212      130      135      140
214 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
215 145      150      155      160
217 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
218      165      170      175
220 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
221      180      185      190
223 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala
224      195      200      205
226 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
227      210      215      220
229 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
230 225      230      235      240
232 Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr
233      245      250      255
235 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
236      260      265      270
238 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
239      275      280      285
241 Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
242      290      295      300
244 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
245 305      310      315      320
247 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
248      325      330      335
250 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
251      340      345      350
253 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
254      355      360      365
256 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
257      370      375      380
259 (2) INFORMATION FOR SEQ ID NO: 3:
261 (i) SEQUENCE CHARACTERISTICS:
262 (A) LENGTH: 1155 base pairs
263 (B) TYPE: nucleic acid
264 (C) STRANDEDNESS: single
265 (D) TOPOLOGY: linear
W--> 267 (ii) MOLECULE TYPE: DNA
269 (iii) HYPOTHETICAL: NO
271 (iv) ANTI-SENSE: NO
273 (vi) ORIGINAL SOURCE:
274 (A) ORGANISM: Brassica napus

```

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/643,579
 DATE: 09/14/2000
 TIME: 16:49:22

Input Set : A:\Cpg.pto
 Output Set: N:\CRF3\09142000\I643579.raw

```

276 (vii) IMMEDIATE SOURCE:
277 (B) CLONE: IMC129
279 (ix) FEATURE:
280 (D) OTHER INFORMATION: G to A transversion
281 mutation at nucleotide 316
282 of the D form
C--> 284 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
286 ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAA AAG TCT 48
287 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
288 1 5 10 15
290 GAA ACC GAC AAC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT 96
291 Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
292 20 25 30
294 GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG 144
295 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
296 35 40 45
298 ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC 192
299 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ala Ser
300 50 55 60
302 TGC TTC TAC TAC GTC GCC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT 240
303 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
304 65 70 75 80
306 CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAG GGC TGC GTC 288
307 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
308 85 90 95
310 CTA ACC GGC GTC TGG GTC ATA GCC CAC AAG TGC GGC CAC CAC GCC TTC 336
311 Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe
312 100 105 110
314 AGC GAC TAC CAG TGG CTG GAC GAC ACC GTC GGC CTC ATC TTC CAC TCC 384
315 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
316 115 120 125
318 TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT CGA CGC CAC 432
319 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
320 130 135 140
322 CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT GTC CCC AAG 480
323 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
324 145 150 155 160
326 AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC AAC CCT TTG 528
327 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
328 165 170 175
330 GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCT TTG 576
331 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
332 180 185 190
334 TAC TTA GCC TTC AAC GTC TCG GGG AGA CCT TAC GAC GGC GGC TTC GCT 624
335 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala
336 195 200 205
338 TGC CAT TTC CAC CCC AAC GCT CCC ATC TAC AAC GAC CGC GAG CGT CTC 672
339 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
340 210 215 220

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/643,579

DATE: 09/14/2000
TIME: 16:49:23

Input Set : A:\Cpg.pto
Output Set: N:\CRF3\09142000\I643579.raw

L:5 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]
L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:65 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:185 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:284 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:267 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3, Value=[DNA]
L:393 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:487 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:475 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5, Value=[DNA]
L:596 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:695 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:678 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7, Value=[DNA]
L:804 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:888 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:902 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:916 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:930 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:944 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:958 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:972 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:986 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1016 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1018 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/643,579

DATE: 09/06/2000
 TIME: 11:53:03

Input Set : A:\BB1334A Corrected Seq Listing.txt
 Output Set: N:\CRF3\09062000\I643579.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
 C--> 5 (i) APPLICANT: RICHARD MARTIN BROGLIE
 6 LORIN ROGER DE BONTE
 7 WILLIAM DEAN HITZ
 8 GUO-HUA MIAO
 9 ROBERT STEFAN REITER
 11 (ii) TITLE OF INVENTION: GENES FOR MUTANT MICROSOMAL
 12 FATTY ACID DELTA-12
 13 DESATURASES AND RELATED
 14 ENZYMES FROM PLANTS
 16 (iii) NUMBER OF SEQUENCES: 17
 18 (iv) CORRESPONDENCE ADDRESS:
 19 (A) ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
 20 (B) STREET: 1007 MARKET STREET
 21 (C) CITY: WILMINGTON
 22 (D) STATE: DELAWARE
 23 (E) COUNTRY: U.S.A.
 24 (F) ZIP: 19898
 26 (v) COMPUTER READABLE FORM:
 27 (A) MEDIUM TYPE: FLOPPY DISK
 28 (B) COMPUTER: IBM PC COMPATIBLE
 29 (C) OPERATING SYSTEM: MICROSOFT WINDOWS 95
 30 (D) SOFTWARE: MICROSOFT OFFICE 97
 32 (vi) CURRENT APPLICATION DATA:
 C--> 33 (A) APPLICATION NUMBER: US/09/643,579
 C--> 34 (B) FILING DATE: 22-Aug-2000
 35 (C) CLASSIFICATION:
 37 (vii) PRIOR APPLICATION DATA:
 38 (A) APPLICATION NUMBER: 08/256,047
 39 (B) FILING DATE: NOVEMBER 17, 1992
 41 (viii) ATTORNEY/AGENT INFORMATION:
 42 (A) NAME: Lynne M. Christenbury
 43 (C) REFERENCE/DOCKET NUMBER: BB-1334-A
 45 (ix) TELECOMMUNICATION INFORMATION:
 46 (A) TELEPHONE: (302) 992-5481
 47 (B) TELEFAX: (302) 892-7949
 48 (C) TELEX:

Does Not Comply
 Corrected Diskette Needed
 Error was edited

ERRORED SEQUENCES

990 (2) INFORMATION FOR SEQ ID NO: 17:
 992 (i) SEQUENCE CHARACTERISTICS:
 993 (A) LENGTH: 5 amino acids
 994 (B) TYPE: amino acid
 995 (C) STRANDEDNESS:

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/643,579

DATE: 09/06/2000
TIME: 11:53:03

Input Set : A:\BB1334A Corrected Seq Listing.txt
Output Set: N:\CRF3\09062000\I643579.raw

996 (D) TOPOLOGY: linear
998 (ii) MOLECULE TYPE: peptide
1000 (iii) HYPOTHETICAL: YES
1002 (iv) ANTI-SENSE: NO
1004 (v) FRAGMENT TYPE: internal
1006 (ix) FEATURE:
1007 (A) NAME/KEY: Modified-site
1008 (B) LOCATION: 2
1009 (D) OTHER INFORMATION: /product= "Asp or Glu"
1011 (ix) FEATURE:
1012 (A) NAME/KEY: Modified-site
1013 (B) LOCATION: 4
1014 (D) OTHER INFORMATION: /product= "Ala or Gly"
C--> 1016 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
W--> 1018 His Xaa Cys Xaa His
1019 1 5
E--> 1021 17
E--> 1023 XX-XXXX
E--> 1026 17

*Extraneous material at end of file
needs to be deleted.*

VERIFICATION SUMMARY

DATE: 09/06/2000

PATENT APPLICATION: US/09/643,579

TIME: 11:53:04

Input Set : A:\BB1334A Corrected Seq Listing.txt

Output Set: N:\CRF3\09062000\I643579.raw

L:5 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]
 L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
 L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
 L:65 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:185 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:284 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:267 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3, Value=[DNA]
 L:393 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:487 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:475 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5, Value=[DNA]
 L:596 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:695 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:678 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7, Value=[DNA]
 L:804 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:888 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:902 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:916 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:930 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:944 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:958 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:972 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:986 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:1016 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:1018 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:1021 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
 L:1023 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:1023 M:330 E: (2) Invalid Amino Acid Designator, 1
 M:332 Repeated in SeqNo=17
 L:1026 M:203 E: No. of Seq. differs, LENGTH:Input:5 Found:6 SEQ:17